

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:51:20 ; Search time 35.44 Seconds

(without alignments)
84.051 Million cell updates/sec

Title: US-09-785-059-2

Perfect score: 148

Sequence: 1 RVIRVQACRAIRHIVRIQGLRLRVV 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	75.7	861	1 VCLJLV	env polypotein pr
2	102	68.9	846	1 S21990	env polypotein pr
3	102	68.9	846	1 VCLJND	env polypotein pr
4	101	68.2	851	1 S33985	env polypotein pr
5	101	68.2	856	1 VCLJH3	env polypotein pr
6	101	68.2	856	1 VCLJVL	env polypotein pr
7	101	68.2	856	1 VCLJ3W	env polypotein pr
8	99	66.9	854	2 S13288	env polypotein pr
9	98	66.2	358	2 S22002	env polypotein pr
10	98	66.2	853	2 S54384	env polypotein pr
11	97	65.5	358	2 S22000	env polypotein pr
12	97	65.5	358	2 S70417	env polypotein pr
13	97	65.5	852	2 T12016	env polypotein pr
14	94	63.5	357	2 S22006	env polypotein pr
15	94	63.5	855	1 VCLJAJ	env polypotein pr
16	93	62.8	852	1 VCLJBR	env polypotein pr
17	90	60.8	357	2 S21994	env polypotein pr
18	86	58.1	357	2 S22004	env polypotein pr
19	86	58.1	859	1 VCLJMN	env polypotein pr
20	85	57.4	358	2 S21998	env polypotein pr
21	85	57.4	861	1 VCLJSC	env polypotein pr
22	84	56.8	856	1 A44963	env polypotein pr
23	83	56.1	843	1 H44001	env polypotein pr
24	83	56.1	868	1 VCLJH4	env polypotein pr
25	82	55.4	357	2 S21996	env polypotein pr
26	82	55.4	357	2 S21992	env polypotein pr
27	78	52.7	847	2 T09448	env polypotein pr
28	78	52.7	847	2 S13289	env polypotein pr
29	77	52.0	859	2 T01672	env polypotein pr

30	77	52.0	861	1 VCLJKB	env polypotein pr
31	75	50.7	855	1 VCLJZR	env polypotein pr
32	70	47.3	854	1 VCLJSI	env polypotein pr
33	64	43.2	863	2 A53034	env polypotein pr
34	58	39.2	877	2 S49197	env polypotein pr
35	56	37.8	859	2 S24571	env polypotein pr
36	54.5	36.8	864	1 VCLJG4	env polypotein pr
37	49.5	33.4	153	2 F86331	env polypotein pr
38	49	33.1	234	2 A87337	env polypotein pr
39	49	33.1	292	2 AG0791	env polypotein pr
40	49	33.1	386	2 F82721	env polypotein pr
41	49	33.1	456	2 C82785	env polypotein pr
42	49	33.1	855	2 A45713	env polypotein pr
43	49	33.1	858	1 VCLJG2	env polypotein pr
44	49	33.1	1512	2 S72354	env polypotein pr
45	48.5	32.8	92	2 S13132	env polypotein pr

ALIGNMENTS

RESULT 1

VCLJLV

env polypotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)

N:Alternate names: coat polypotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03975

R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.

Cell 40, 9-17, 1985

A:Title: Nucleotide sequence of the AIDS virus, LAV.

A:Reference number: A90866; M01D:85099333

A:Accession: A03975

A:Molecule type: DNA

A:Residues: 1-861 <MAT>

A:Cross-references: GB:K02013; NID:q326417; PIDN:AAB59751.1; PID:q326424

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-861/Product: exterior membrane glycoprotein #status predicted <TM>

F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,337,344,361,391,397,402, F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 75.7%; Score 112; DB 1; Length 861;

Best Local Similarity 85.7%; Pred. No. 2.4e-07;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHIVRIQGLRLRV 28

DB 833 RVIRVQACRAIRHIVRIQGLRLRV 860

RESULT 2

S21990

env polypotein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 20

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C:Accession: S21990; S70423

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S21990

A:Molecule type: DNA

A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.2%; Score 101; DB 1; Length 856;
Best Local Similarity 82.1%; Pred. No. 7, 2e-06;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLERIL 28
DB 828 RVIEVVGAVRAIRHIVRIROGLERIL 855

RESULT 7

env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1; HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C:Accession: A24774
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.; Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the env
A:Reference number: A24774; MUID:86218077
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <Sig>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,456

Query Match 68.2%; Score 101; DB 1; Length 856;
Best Local Similarity 78.6%; Pred. No. 7, 2e-06;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLERIL 28
DB 828 RVIEVVGAVRAIRHIVRIROGLERIL 855

RESULT 8

env protein - human immunodeficiency virus type 1
S13288
C:Species: human immunodeficiency virus type 1; HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13288
R:O'Brien, W.A.; Kovacs, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A. Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
C:Superfamily: type E retrovirus env polypeptide

Query Match 66.9%; Score 99; DB 2; Length 854;
Best Local Similarity 78.6%; Pred. No. 1, 3e-05;
Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLERIL 28
DB 826 RVIEVVGAVRAIRHIVRIROGLERIL 853

RESULT 9

S22002

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1; HIV-1
A:Variety: isolate 3L
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S22002; S70418
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S22002
A:Molecule type: DNA
A:Residues: 1-358 <STE1>
A:Cross-references: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209
A:Accession: S70418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333, 'X', 335-358 <STE2>
A:Cross-references: EMBL:X61352; NID:g60186
C:Superfamily: type E retrovirus env polypeptide

Query Match 66.2%; Score 98; DB 2; Length 358;
Best Local Similarity 71.4%; Pred. No. 8, 6e-06;
Matches 20; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLERIL 28
DB 330 RVIEVVGAVRAIRHIVRIROGLERIL 357

RESULT 10

envelope polypeptide - human immunodeficiency virus type 1
S54384
C:Species: human immunodeficiency virus type 1; HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C:Accession: S54384
R:Rhodes, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: polypeptide

Query Match 66.2%; Score 98; DB 2; Length 853;
Best Local Similarity 67.9%; Pred. No. 1, 8e-05;
Matches 19; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLERIL 28
DB 825 RVIEVVGAVRAIRHIVRIROGLERIL 852

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1
S22000
C:Species: human immunodeficiency virus type 1; HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S22000

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <SNE>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polypeptide

Query Match 65.5%; Score 97; DB 2; Length 358;
Best Local Similarity 75.0%; Pred. No. 1.2e-05;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
DB 330 RVIEVQXRCRAIRHIVRIROGLRSL 357

RESULT 12
S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C:Date: 10-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S70417
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185
C:Superfamily: type E retrovirus env polypeptide

Query Match 65.5%; Score 97; DB 2; Length 358;
Best Local Similarity 75.0%; Pred. No. 1.2e-05;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
DB 330 RVIEVQXRCRAIRHIVRIROGLRSL 357

RESULT 13
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T12016
R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in South Africa
A:Reference number: Z17379; MUID:98178716
A:Accession: T12016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-852 <MCC>
A:Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide

Query Match 65.5%; Score 97; DB 2; Length 852;
Best Local Similarity 75.0%; Pred. No. 2.5e-05;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
DB 824 RVIEVQXRCRAIRHIVRIROGLRSL 851

RESULT 14
S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70420; S22006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
A:Experimental source: patient L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypeptide

Query Match 63.5%; Score 94; DB 2; Length 357;
Best Local Similarity 71.4%; Pred. No. 3e-05;
Matches 20; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
DB 329 RVIEIQRVAVRAIRHIVRIROGLRSL 356

RESULT 15
VCLJAZ
env polypeptide precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03976
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown
Science 227, 484-492, 1985
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A:Reference number: A04003; MUID:85090453
A:Accession: A03976
A:Molecule type: DNA
A:Residues: 1-855 <SAN>
A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,
F:610,624,636,815/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 63.5%; Score 94; DB 1; Length 855;
Best Local Similarity 75.0%; Pred. No. 6.3e-05;
Matches 21; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
DB 827 RVIEVQXRCRAIRHIVRIROGLRSL 854

Search completed: August 14, 2002, 10:51:21
Job time: 307 sec